10

15.4

20

1

25

30

- (1) GENERAL INFORMATION:
 - (iii) NUMBER OF SEQUENCES: 23
- (2) INFORMATION FOR SEQ ID NO:1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6689 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic) human
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene
 - (B) LOCATION: 17p13.1
 - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ggcctcccaa agtgctggat tacaggcgtg agtcaccgcg cctggtcccc tgtcttcttt

aagaaagctc agcggacctt tttccttctt ggggtggaac aaaaagccaa atctagcaca

accetgggca ggggcccaga atcactggaa gcaaaggtgg atgggatagg aggcgaggct 181

gcctgtggac cacaggcccg gcccgagtgg ctctgatgag aagccggggc gcctaggtca 241

ccgccccac cgtctgcct tcccccact cctcctggct gggtaaatcc cagagtctca 301

gccgcctaag tgtcttcccc ggaggtgaga ttatctccgc ctgtgctgga cacctccctt 361

tctcctgcag ccatggatgc cgctctgctc ctgaacgtgg aaggggtcaa gaaaaccatt

ctgcacgggg gcacgggcga gctcccaaac ttcatcaccg gatcccgagt gagtggggcc 481

cctccggagc agacagggtc ccccacagca gctttcaaca ttccaggtgt gccccaaggc

	541					
	actgtaaaca	gctttcagct	gtgccaaaaa	aacagccagg	cagccccagc	gctgggcctc
	601					
	cggggagctc	ccagcgttta	cccattcagg	gggcattttt	ggtactttgc	agattcaact
5	661					
	ttagcatggg	ctgaggggaa	gggcttttgg	gaattttctg	gggccctaaa	tgttgagtga
	721					
	_	agtccgagga	gtcttggtat	ttgtccccaa	atgtctgtta	ggcttccctg
10	781					
10		tgcgtctgtg	gctacagaat	tegggetttg	gccaggcgag	geggeteeeg
	841		~~~~~~~~	atagagagat	astasaatas	agagttggag
		cagcactttg	ggaggccaag	atyggdagat	catgaggtca	agageeegag
n of marking	901	aasaatata	aaaccccatc	tctactcaaa	atacaaaaat	tanccanato
15_	961	ccaacacgcg	adaccccatc	cccaccyaaa	acacaaaaac	cagocagacg
		cctqtaatcc	cagttcagat	actcaggaga	cttgaggcag	gagaatcact
	1021					3 3
The second secon		aggtggaggt	tgcagtgagc	cgagatcata	ccactgcact	ccaacctggg
200	1081					
20	caacagagtg	agactctgtc	tcagaaaaaa	aaaaaaaaa	aagaactcgg	gcttacttga
To the second se	1141					
	ggaaggattt	ctggacgcac	agggctgtgg	ggagtggaat	ggggtctgta	gggaggggtg
Company	1201					
	ggtccctcct	ccctgggggg	tgcaggcagg	gtggaggtgc	tccaggggtc	tgaggcatct
25	1261					
		actgagtgag	ctgaccctgg	ggacagccct	gggtgtcggt	ggcaaggggg
	1321					
		cgggccttga	acagtgtgtc	tagagcagag	tgcaccgtct	cggtgactag
	1381					<i>L</i>
30		atttccgcac	catgaaatgt	gatgaggagc	ggacagtcat	tgacgacagt
	1441	aacaaaaat	gangatanta	2+444222242	tattassaat	casaatataa
	1501	godayoddat	geacateate	accyyaaaca	tgttcaagct	cgaggcccgg
		ttacctccat	acagatacac	aaaataacca	agttctggtg	cgacaccatc
				-, -, -, -, -, -, -, -, -, -, -, -, -, -	~~~~~~~~~	, ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~

	1561					
	gtaagtaggc	cctgcgcgcc	tgtctcctgg	gactagtctt	ttctgggctc	acccacccgc
	1621					
	tttgcggggc	tgctgtgttt	cgggaaagct	gggactcaag	cgaagctttg	caaagccagt
5	1681					
	cctgcaaact	tattccccac	cgtgtgcatg	tgaagatgga	gggaacaagg	gctggaaggg
	1741					
	gtgacccatg	ctgtggctgg	ctggtgggga	gcagggctat	gaccagcagg	agtgagctgg
	1801					
10	cccacttcac	agtcctcaca	tctgtgtgtg	tgtgtgtgtg	tgtgtgtgtg	tgtgtgtgtg
	1861					
	tgtgtgtgtg	agagagagag	agagagagag	agagagnnnn	nnnnntagc	cttaggactt
	1921					
The same	attgcagaga	ccaacaccta	acaatgtaat	caggcagcca	gtgcaggaca	taaataagta
15	1981					
real baseline real baseline real baseline real	aggcagtgtg	ctttgggcca	caaaagcacg	ctcagcttgc	tggaagccat	gggtgccgag
THE SECTION OF THE SE	2041					
A ST SHAPEN	ctgggggctg	ctgagtcagg	gccaaagggg	gcccctccct	gcagtaagct	ggttctgggg
#i	2101					
20=		ccttggtcca	gctcttaatc	ccaacaggct	caacagccat	ctgcttgtct
	2161					
		gaggcagaag	gcatttcggg	ctaatcccgg	ccggtggggc	gggcagggtg
To the state of th	2221					
25		ctgtgctggt	gacctggagg	cagagetgaa	ctgctgcata	gagtttcagc
25	2281		. h a h a a a a a a	- ~+ ~ a+ ~ a+	ant at an ann	accatacaa
		cacatgttgc	atgtggggee	agtgetgggt	Catctcagaa	geeggeedaa
	2341	tataaaaaaa	aataattaaa	assatasaa	cccaccatac	atacaccacc
	ggagatgggt 2401	tctcagggag	cctagttggg	gaaactgagg	cccagcacac	acacagcagg
30		gccgcacggc	ggatetteee	agccctcctt	caticccaagg	gtggcaaact
30	2461	geegeaegge	ggacccccc	ageceeeee		5055000000
		actaactaaa	actataataa	gccagaticta	tatctgcacc	atctcattta
	2521	2002200244	J50-50	J J	2 2 3 2 3 2 3 2 3	
		cagecetaat	atcgaacagg	aqcaacccaq	qqaactqaqt	ttcagagaag
			3 33	5	55 5 5	

	2581					
	tgcagagacc	tgggctcacc	gctaacctgc	agcactgcca	ggacaccaaa	gcgactctct
	2641					
	tggaccctgg	agtcctgctc	cttctactgc	cccacactgc	ccttcctgcg	agtcataggc
5	2701					
	tttgcagagg	tcagggtttc	cctggggcag	agatgtgtta	cagtggacca	caagggccag
	2761					
	aagaggcagc	cggaggctaa	cagcatatgg	cctctggagc	caggtttgaa	tcctggctgc
	2821					
10	gtcatttcct	agctgtgtga	ccttaagcaa	gttgcttgcg	tctctgggct	gtagtttccc
	2881					
	catccgtaaa	atgggataat	agtgcctgcc	ttgaattgtc	ataaggattg	aaggggctca
	2941					
2.01 minutes 2.02 minutes 2.03	taacagtgtg	aagtgctttg	cctggcacac	agttaaccac	agttagtatg	agtggcatag
15	3001					
188 Section 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		ggattcctcc	caggaggggc	tctgagtgga	ggccttttat	ggcccaccta
THE THE PARTY OF T	3061					
		ggtagcctgg	atgccatcca	tccgtttatc	cccacagcac	acgggggtct
33	3121		at an agangn	+~~~~~~	annaanaaa	agagagtaga
203		rteeeggage	ctgaggcaga	Lggcccaggg	caaggacccc	acagagugge
	3181	ataggggta	aaaaaatat	taaaataaaa	cacgctgggc	tacqaqqaqq
Los cardina Antis manages, Company	3241	grgcgggccg	gecaacacge	cegeecacca	cacgoogggo	cacgaggacc
System magnetic System magnetic system magnetic ()		acadaaddad	cctcagcctc	taatetttat	gatcgagctg	ctacaaataa
25	3301	9049449		- 555-	55 5 5	3 33 33
		ggcagggctg	gagggctgtg	ccagcactgg	agagggacag	cgggcatcat
	3361					
	gggcaccccc	accccactgg	ccactggaca	gtgccctgtt	tctgtttaga	taatacgaga
	3421					
30	gggttcataa	gccatgggag	aatacgaatt	tgaaaaaaaa	gtcctctgat	ttttccacaa
	3481					
	gaaaagtcct	ttggtgctgg	gcatggtggc	ccacgcctgt	aatcctagca	ctttgggagg
	3541					
	ccgagggggt	tggatcacct	gaggtcagga	gttcgaagac	cagcctggcc	aacatggtaa

	3601					
	aaccccgtct	ctattaaaaa	cacaaaaatt	aaccgggtgt	ggtggtgcat	gcctgtaatc
	3661					
	aatcccagct	acttgggaat	ttgaggcatg	agaattgctt	gaacctggaa	gtggaggttg
5	3721					
	cagtgagcag	agatcatgtc	agtgcatttt	aacctgggtg	acagagtgag	actccatgtc
	3781					
	caaaaaaaag	aaaaaaaaa	aaagtccact	tggaaccagt	ttttaaaaat	gtgattcatt
	3841					
10	ttcattgtgg	aggcatttta	tccacttcca	ctttcatttt	caggagttgg	agattataac
	3901					
	cgcctccttg	gttcctgtgg	tttgtgggtt	cagacttggt	tctctngtgg	cgggagaggc
	3961					
one suppose	tgcatggaac	tccccacatc	ctcccaacca	ggagccccag	agtgattggc	agcgcgtgtt
15	4021					
15 Will have been been been been been been been be	tgtggattgg	tgagagaggg	ttagggccag	ggtcaaggtc	aggtcaggac	tcagcttatg
75 mars	4081					
	gccaagactg	aggctcagcc	tgagagctat	gtgggtgaat	aaaataaaat	aagaactgtg
	4141					
20	tcaaccaagg	gccccttaca	ggcttgctgt	cacagttgtg	tggtctgtgc	actgcacaag
	4201					
74	gtgcaccggc	atctcctcca	aggtgctcat	tatagacatt	gtatattggt	atttccataa
	4261					
	tgagaagttt	ccagcagatg	gcaatagtgt	attgttctaa	caaaacgagt	attcgtgaca
25	4321					
	attttctgaa	tattagaagt	gaagtgtctt	gatgaacggg	caccttttcc	tagtttgcac
	4381					
	aaagacattg	atttagggca	gggttttcgg	cgttgttgct	tctttccctt	gtctgtatgc
	4441					
30		caagcatgac	ttcagggaga	tgtgccacag	ggtcctgttt	ttcgggtctc
	4501					
		caggcccctg	gggtccctgc	ctcactgacc	tgcagctctg	gggccaggtt
	4561					
	gatgccccga	gtgattacca	gagggagacc	tggaacctga	gcaatcatga	gaagatgaag

	4621					
	gcggtgcccg	tcctccacgg	agagggaaat	cggctcttca	agctgggccg	ctacgaggag
	4681					
	gcctcttcca	agtaccagga	ggccatcatc	tgcctaagga	acctgcagac	caaggtcaga
5	4741					
	ggccgctggc	caggggtggg	aagtggcgct	gactctgggg	ggcctgccca	gtgccggcca
	4801					
	gggtggggcg	ggggttgggc	agctgcctga	ggtcatggct	gaccttctcc	ctgggcagga
	4861					
10	gaagccatgg	gaggtgcagt	ggctgaagct	ggagaagatg	atcaatactc	tgatcctcaa
	4921					
	ctactgccag	tgcctgctga	agaaggagga	gtactatgag	gtgctggagc	acaccagtga
	4981					
15		caccacccag	gtgcgcgggg	ctgcaggggc	ggacagtgag	ggggcgccca
15_	5041					
All States		acggagacac	ctgccatagc	cttcctggac	ttttctttcc	accccaccag
di banda	5101					
######################################		cttgtctcca	cccagccggg	tttccccgag	tgtgtaactg	aattgtgggt
Annua from an appending control transferre	5161					
20-		cagtgcttgg	cgcggggcgg	cctttatttt	aatgtgtgtt	tgaacactta
	5221					L.L
		tcgccaagct	tgtgatttca	gcggaacggt	aaacaggcgt	ttaaaaagag
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	5281			1		+ +~~~~~+
		tatagggaaa	aatattatga	tgtcggtact	agtactggtg	ttgcgaggat
25	5341		L L L		~~+ ~~ ~~ ~	22222±222
		agtactagat	tgacttaatg	ctegaategt	gctcacagta	addaUdLCCd
	5401			+ a+ a a a + + + a	++ >+ a+ a+ a >++	taataataat
		catgcatcag	geacacgreg	tetgegttta	ttatctcatt	taattettat
20	5461	a+ ca caa+ a+	anagangata	anaaannaa	aaaataaaaa	ttatctaatt
30		attattat	gagggaggcg	cagggaaagg	ggcctgaagg	ccacccaacc
	5521	atotooassa	22+22222	agttatgaat	ataaaattaa	taacaaaaaa
		Clacadyada	aataaaacaa	ayıtatyadı	ataaaattac	ccacayyycc
	5581	~~~~~~~~ ~	t > 0 t ~ 0 t > t t	atontonton	tctccatctt	acacttcacc
	ıladadaqqa	9a99a99a99	<i>uaulyulall</i>	alyallalla	ucucualul	acayiigayy

	5641					
	aaaccgaggg	atgggggata	cagagaggtt	aaggatcatg	gcggggctga	gggtcttgga
	5701					
	ggctggtgag	tcccagctgg	gctggggctg	cctctgaggc	tgggaaggga	gctgtagctg
5	5761					
	gatgctccct	gctccccaca	ggcatcgtga	aggcctacta	cgtgcgtgcc	cgggctcacg
	5821					
		gaatgaggcc	gaggccaagg	cggacctcca	gaaagtgctg	gagetggage
	5881					
10		gaaggcggtg	cgcagggagc	ttgaggctgc	tggagaaccg	catggcggag
	5941				1	
		ggagcggctg	cgctgccgga	acatgctgag	ccagggtgcc	acgcagcctc
-17 07%	6001			201001	agaggagt	aasasaasa
12		acccacagag	ccaccegeae	agreatecae	agagccacct	gcagagccac
13	6061	atataaaaa	atataaaaa	aacacactac	agagccagcc	acadadccac
	6121	accegeagag	ctgtctgtag	ggccccccgc	agageeagee	acagagecae
		agggcactcg	ctacagcact	gagccccctg	aggcccacag	ccacccaqqc
.	6181	4333040003		JJ	33 3	33
20		tggcctggtc	acttctggtt	cgattgacca	ggatcgtggt	gtcacttttt
To see the second secon	6241					
	aaaatttaaa	attaattttt	gaaatcaaag	tcagacacac	ccatggtaaa	aaaaaaaaa
The second secon	6301					
•	aaaacaatcc	caagggtaca	gaagagctta	tgaataaaag	tagttttctc	ctctacccct
25	6361					
	ctcattcctt	ccgtgccatg	gttttaattg	accctgtttt	taattcttct	ggtagttttc
	6421					
	tctatttcca	agtaatctgt	ttaaatcagt	ttctagattt	taccccatgt	caatgacaaa
	6481					
30		atgctctgat	cctttctcat	gcctgatacc	cctccctgtc	tccccatttt
	6541					
		atttgggggt	catctcggtg	atttttgtaa	ctttacgcag	gacacttaga
	6601	a+ aa===+==	a+++ a ~+ ~~	~+ ~+ ~ ~ + ~ · +	aggetgagg	2000000000
	uctetetada	atcccactqa	ciliagiaga	guculgalat	agggtgggca	aquicucyaca

```
5
```

15.

20=

25

30

```
(2) INFORMATION FOR SEQ ID NO:2:
```

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1119 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA Baboon
- (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene
 - (B) LOCATION:
 - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
atggatgccg ctctgctcct gaacgtggaa ggggtcaaga aaaccattct gcacggaggc
acgggcgagc tcccaaactt catcaccgga tcccgagtga tctttcattt ccgcaccatg
aaatgtgatg aggagcgcac ggtcatcgac gacagccggc aggtggacca gcccatgcac
atcatcatcg ggaacatgtt caagetegag gtetgggaga teetgeteae etecatgagg
gtgcacgagg tggccgagtt ctggtgcgac accatccaca cgggggtcta ccccatcctg
tcccggagcc tgcggcagat ggcccagggc aaggacccca cggagtggca cgtgcacaca
tgcgggctgg ccaacatgtt cgcctaccac acactgggct acgaggacct ggacgagctg
cagaaggagc ctcagcctct gatctttgtg atcgagctgc tgcaggttga cgccccgagt
gattaccaga gggagacctg gaacctgagc aatcatgaga agatgaaggt ggtgcccgtc
ctccacggag agggaaatcg gctcttcaag ctgggccgct acgaggaggc ctcttccaag
taccaggagg ccatcatctg cctaaggaac ctgcagacca aggagaagcc atgggaggtg
cagtggctga agctggagaa gatgatcaac accctgaccc tcaactactg ccagtgcctg
ctgaagaagg aggagtatta cgaggtgctg gagcacacca gtgacattct ccggcaccac
ccaggcatcg tgaaggccta ctatgtgcgt gcccgggctc acgcagaggt gtggaatgag
gccgaggcca aggcggacct ccagaaagtg ctggagctgg agccatccat gcagaaggcg
gtgcgcaggg agctgaggct gctggagaac cgcatggcag agaagcagga ggaggagcgg
ctgcgctgcc ggaacatgct gagccaggga gccacgcagc ctcccacaga gccaccggca
gagececaca cageaceace tgeggagetg tecaeaggge caeetgeaga gecaeeegea
```

gageteece tgteeceagg geacteactg cageactga

	(2) INFORMATION FOR SEQ ID NO:3:
	(i) SEQUENCE CHARACTERISTICS:
5	(A) LENGTH: bases
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: cDNA Chimpansee
10	(ix) FEATURE:
	(A) NAME/KEY: AIPL1 gene
	(B) LOCATION:
	(D) OTHER INFORMATION: produces aryl-hydrocarbon
and standard	receptor interacting protein-like 1
1 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
tgtcegca	agdggatgctgctgtgtgtgtttgtcagtgaatgtgcaacgccttgtaccaagtggattttgctgctgggggctagtgggc
10 miles	(2) INFORMATION FOR SEQ ID NO:4:
Trees Trees Control	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: bases
ed all well from the	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: cDNA Cow
25	(ix) FEATURE:
	(A) NAME/KEY: AIPL1 gene
	(B) LOCATION:
	(D) OTHER INFORMATION: produces aryl-hydrocarbon
	receptor interacting protein-like 1
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
	atggatgccactctgctcctgaatgtggaagggatcaagaaaaccattctgcatgggggcacagg
	ggacctcccaacttcattactggagcccgagtgacctttcatttccgaaccatgaaatgtgatg
	aggagcggacggtgatagacgacagcaggtgggccatcccatgcacatcatcattgggaac

 $\verb|atgttcaagctggaggtctgggagatcttgctgacgtccatgcgggtcagcgaggtggccgagtt|\\$

30

5

10

ttggtgcgacaccatccacacaggggtctaccccatcctgtcccggagcctgcggcagatggcgg agggtaaggaccccacagagtggcacgtgcacacgtgtggcttggccaacatgttcgcttaccac acgctgggctacgaggacctggacgagctgcagaaggagcctcagccactgatcttcataatcga gttgctgcaggtcgaggccccgagccagtaccagagggagacctggaacctgaataaccaggaga agatgcaggcggtgcccatcctccatggagaaggaaaccggctcttcaagctgggccgctacgag gaggcctccaacaagtaccaggaagccatcgtctgcctgaggaacctgcagaccaaggagaaacc ctgggaggtgcagtggctgaagctggagaagatgatcaacaccctgatcctgaactactgtcagt gtctgctgaagaaggaggagtactacgaggtgctggaacacactagtgacatcctccggcatcac ccaggcatcgtgaaggcctactatgtgagggcccgggctcacgccgaggtgtggaatgaggcgga agccaaggcggatctggagaaagtgctggagctgtgcatgcgtgcagaggcggtgcagaggg agctgaggctgctggagaaccggctggaggagaaacgcgaggaggagcgactgccggaac atgctgggctagtgcgcaggcgccaagcctcctgcctccgcccccgcycctccaccccccaa aaaaaaaaaaaattttt

- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA Dog
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene
 - (B) LOCATION:
 - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

tgtacgggggcaccggcgagctcccaaacttcctcacggggtcccgggtcatctttcacttccgc acaacgaaatgcgacgaggcgggacagtgatcgacgacagcaagcgtgtggggccatcccatgca $\verb|catcatcatcgggaacatgttcaagctggaggtctgggaggtgctgctgacatccatgcgcgtgg|\\$ gcgaggtggccgagttctggtgcgactctattcacacaggagtctaccccatcctgtcccggagc ctgcggcaggtggcggagggcaaggaccccactgagtggcatgtacacacgtgcggcttggccaa catgtttgcctatcacacgctgggctacgaggacctggacgagctacagaaggagccgcagcccc tcatcttcatgatagagctgctgcaggtggaggccccaagtgagtaccagagggagacgtggagc

30

ctgaacaatgagagaagatgcagcggtacccatctcatggagaggggaaccggctcttcaagctg ggccgctacaatgatgcctccaccaagtaccaggagccatcgtctgctgaggaacctgcagacca aggagaagcctgggaggtgcagtggctaaagctggagaagctgatcaacaccttgattctcaact actgccagtgtctgctgaagaaggaggagtactacgaggtgctggagcacactagcgacatcctg cggcttcacccaggaatcgtgaaggcctactacgtgcgcgcccgggctcacgcggaggtgtggaa tgcgcagggagctgcggcttctggaaaatcgcctggaggaaaagcgggaggaggagcggctgcgc tgccggaacatgcta

10

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: bases

(2) INFORMATION FOR SEQ ID NO:6:

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA mouse
- (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene
 - (B) LOCATION:
 - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

atggacgtctctctactcctcaatgtggagggtgtcaagaagaccattctgcatggggggacagg agagetececaaetteateaetggetecagagtgaeettteattteegaaeaatgaagtgtgatg aagaacgcacggtgatcgatgacagcaagcaggtgggccagcccatgagcatcatcatcggcaac atgttcaagctggaggtgtgggagacgctgctgacctccatgcggctgggcgaggtggctgagtt ctggtgcgacaccattcacacaggggtctaccctatgttgtcccgcagtctgcggcaggtggctg agggcaaggaccccacaagctggcatgtgcacacgtgcgggttggccaacatgtttgcataccac acgctgggctacgaggacctggatgagctgcagaaagagccacagcctcttgtcttcctgtatga actgttgcaggtggaggccccaaatgagtaccagagggagacgtggaacctgaataatgaagaga ggatgcaggcggtacctcttcttcatggagaaggcaacaggctctacaagctgggacgctatgat $\verb|caggccgccaccaagtaccaggaggccattgtgtgcctgaggaaccttcagaccaaggagaagcc|\\$ ctgggaggttgagtggctgaagctggagaagatgatcaacccctgatcctcaactactgccagt gcctgctgaagaaggaggagtactacgaggtgttggagcacaccagcgacattctacgacaccac

5

30

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA Rhesus monkey
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene
 - (B) LOCATION:
 - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

30

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA Squirrel monkey
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene
 - (B) LOCATION:
 - (D) OTHER INFORMATION: produces aryl-hydrocarbon receptor interacting protein-like 1
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

atggatgccgctctgctcctgaacgtggaagggtcaagaagaccattctgcacggggcacggg cgagctcccaaatttcatcaccggatcccgagtgatctttcatttccgcaccatgaaatgtgatg aggagcggacggtgattgacgacagcagggaggtgggccagcccatgcacatcatcatcgggaac $\verb|atgttcaagctggaggtctgggagatcctgctcacgtccatgcgggtgcgagaggtggccgagtt|\\$ ctggtgcgacaccatccacacgggggtctaccccatcctgtcccggagcctgcggcagatggccc agggcaaggacccgacggagtggcatgtgcacacgtgcgggctggccaacatgttcgcctaccac acgctgggctacgaggacctggatgagctgcagaaggagcctcagcctctgatctttgtgatcga gctgctgcaggttgatgccccaagtgattaccagagggagacctggaacctgagcaatcacgaga agatgaaggtggtgcccgtcctccatggagaaggaaataggctcttcaagctgggccgctacgag gaggcctcttccaagtaccaggaggccatcatctgcctaaggaacctgcagaccaaggagaaacc $\verb|ctgggaggtgcagtggctgaagctggagaagatgatcaataccctgatcctcaactactgtcagt|\\$ $\verb|gtctgctgaagaaggaggagtactacgaggtcctggagcataccagtgacattctccggcaccac|$ ccaggcattgtgaaggcctactatgtgcgcgcccgggctcacgcggaggtgtggaacgaggccga ggccaaggcggacctccagaaagtgctggagctggagccgtccatgcagaaggcggtgcgcaggg agetgaggetgetggagaaccgcatggcggagaagcaggaggaggagcggctgcgctaac atgctgagccagggggccacgtggtcccccgcggagccacccgcagagccacctgcagagtcatc

	(2) INFORMATION FOR SEQ ID NO:9:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 15 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 Met79Thr Mutation	
	(B) LOCATION: 7781	
of the state of th	(D) OTHER INFORMATION: Thr 79 mutation	
To the sale that the sale that the sale to the sale to the sale that the sale to the sale	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
AST DESCRIPTION OF THE PROPERTY OF THE PROPERT	acc tcc acg cgg gtg	15
	Thr	
THE REPORT OF THE PERSON OF TH		
Construction of the Constr	(2) INFORMATION FOR SEQ ID NO:10:	
	(i) SEQUENCE CHARACTERISTICS:	
20 miles and many trains and m	(A) LENGTH: 15 bases	
91 out	(B) TYPE: nucleic acid	
Sin constitution of the co	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 Trp88X mutation	
	(B) LOCATION: 8690	
	(D) OTHER INFORMATION:	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
	gag ttc tga tgc gac	15
	X	

Page 90

(2) INFORMATION FOR SEQ ID NO:11:

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(A) NAME/KEY: AIPL1 Ala197Pro mutation

(ix) FEATURE:

15

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

	(ii) MOLECULE TYPE: DNA (genomic)	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 Ala336del2 mutation	
	(B) LOCATION:	
5	(D) OTHER INFORMATION:	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
	t ccc gca gcc acc	13
	del AG	
10	(2) INFORMATION FOR SEQ ID NO:23:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
15 the rest that the state of t	(D) TOPOLOGY: linear	
2 7	(ii) MOLECULE TYPE: DNA (genomic)	
9,7 E	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 Cys42X mutation	
55 55	(B) LOCATION:	
20	(D) OTHER INFORMATION:	
\$ 2	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
Ş1 -2	atg aaa tga gat gag	15
	X	
25	(2) INFORMATION FOR SEQ ID NO:24:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 Leu257del9 mutation	
	(B) LOCATION:	

	(D) OTHER INFORMATION:	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
		12
	del CTCCGGCAC	
5		
J	(2) INFORMATION FOR SEQ ID NO:25:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 bases	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(ix) FEATURE:	
in same	(A) NAME/KEY: AIPL1 Val33ins8 mutation	
15	(B) LOCATION:	
70 Table 2	(D) OTHER INFORMATION:	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
Cold Contents Cold Contents Cold Contents Cold Cold Cold Cold Cold Cold Cold Cold	gac tag gtg atc ttg tga tct	
3.5 3.5	ins GTGATCTT	
	(2) INFORMATION FOR SEQ ID NO:26:	
To the state of th	(i) SEQUENCE CHARACTERISTICS:	
20 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	(A) LENGTH: 20 bases	
	(B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 IVS1-9G->A Beni	.gn
30	Variants/Polymorphisms	
	(B) LOCATION:	
	(D) OTHER INFORMATION:	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
	CTC AGT GAC TAG	

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 IVS2+66G->C Benign Variants/Polymorphisms
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
 TTT GCC GGG CTG
 G->C
- (2) INFORMATION FOR SEQ ID NO:28:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 IVS2-88C->T Benign Variants/Polymorphisms
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCC TCT CAG GAG C->T

5

10

- (2) INFORMATION FOR SEQ ID NO:29:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 IVS2-14G->A Benign Variants/Polymorphisms
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

 ATC CAT TTA TCC

 G->A
- (2) INFORMATION FOR SEQ ID NO:30:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 IVS2-10A->C Benign Variants/Polymorphisms
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGT TTC TCC CCA

A->C

- (2) INFORMATION FOR SEQ ID NO:31:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 bases

(B) TYPE: nucleic acid

30

5

10

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 IVS5+18G->A Benign Variants/Polymorphisms
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

 AGG AGC GGA CAG

G - > A

- (2) INFORMATION FOR SEQ ID NO:34:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 Asp90His Benign Variants/Polymorphisms
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
 TGG TGC CAC ACC

His

- (2) INFORMATION FOR SEQ ID NO:35:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

	AGT GAC ATT CTC	
	Asp	
5	(2) INFORMATION FOR SEQ ID NO:42:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA Primer	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 primer	
of the control of the	(B) LOCATION:	
15	(D) OTHER INFORMATION:	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
No. Section 1	5'-AAGAAAACCATTCTGCACGG-3'	20
THE STATE OF THE S		
2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	(2) INFORMATION FOR SEQ ID NO:43:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 19 bases	
100 maga.	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
•	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA Primer	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 primer	
	(B) LOCATION:	
	(D) OTHER INFORMATION:	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:	
	5'-TGCAGCTCGTCCAGGTCCT-3'	19
	(2) INFORMATION FOR SEQ ID NO:44:	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(C) STRANDEDNESS: single

(ix) FEATURE: (A) NAME/KEY: AIPL1 gene exon/intron Acceptor splice site 5 (B) LOCATION: (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51: 35 cagagtgcaccgtctcggtgactagGTGATCTTTC 10 (2) INFORMATION FOR SEQ ID NO:52: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) human (ix) FEATURE: (A) NAME/KEY: AIPL1 gene exon/intron Donor splice site (B) LOCATION: (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52: CSACACCATCgtaagtaggccctgcgcgcctgtct 35 (2) INFORMATION FOR SEQ ID NO:53: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 bases (B) TYPE: nucleic acid 30 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) human (ix) FEATURE: NAME/KEY: AIPL1 gene exon/intron Acceptor

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(B) LOCATION: 17p13.1 (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53: 5 qccatccatccqtttatccccacaqCACACGGGGG 35 (2) INFORMATION FOR SEQ ID NO:54: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 35 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) human (ix) FEATURE: (A) NAME/KEY: AIPL1 gene exon/intron Donor splice site (B) LOCATION: (D) OTHER INFORMATION: (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54: GCTGCTGCAGgtggggctggggttggcagggctgg 35 (2) INFORMATION FOR SEQ ID NO:55: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 6689 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: AIPL1 gene exon/intron Acceptor splice site (B) LOCATION: (D) OTHER INFORMATION:

splice site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

30

5

10

- (2) INFORMATION FOR SEQ ID NO:56:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene exon/intron Donor splice site
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

 GCAGACCAAGgtcagaggccgctggccacggggtg 35
- (2) INFORMATION FOR SEQ ID NO:57:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: AIPL1 gene exon/intron Acceptor splice site
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:
 catggctgaccttctccctgggcagGAGAAGCCRT 35
- (2) INFORMATION FOR SEQ ID NO:58:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: nucleic acid

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
	5'-gggccttgaacagtgtgtct-3'	20
	(2) INFORMATION FOR SEQ ID NO:63:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 19 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA Primer	
	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 gene Exon 2 Primer	
	(B) LOCATION: 297	
AND PROMISE TO THE PERSON OF T	(D) OTHER INFORMATION:	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
4.1 minute 4.1 minute 7.1 minute	5'-tttcccgaaacacagcagc-3'	19
15. 15. 10. 10. 10. 10. 10. 10. 10. 10. 10. 10	(2) INFORMATION FOR SEQ ID NO:64:	
j. = H	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 18 bases	
	(B) TYPE: nucleic acid	
in the state of th	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA Primer	
25	(ix) FEATURE:	
	(A) NAME/KEY: AIPL1 gene Exon 3 Primer	
	(B) LOCATION: 364	
	(D) OTHER INFORMATION:	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
30	5'-agtgaggagcaggattc-3'	18
	(2) INFORMATION FOR SEQ ID NO:65:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 bases	

(A) NAME/KEY: AIPL1 gene Exon 4 Primer

(2) INFORMATION FOR SEQ ID NO:70:

Page 117

(ix) FEATURE:

30

- (A) NAME/KEY: Human Aipl1
- (B) LOCATION:
- (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
- 5 MDAALLLNVEGVKKTILHGGTGELPNFITGSRVIFHFRTMKCDE
 ERTVIDDSRQVGQPMHIIIGNMFKLEVWEILLTSMRVHEVAEFWCDTIHTGVYPILSR
 SLRQMAQGKDPTEWHVHTCGLANMFAYHTLGYEDLDELQKEPQPLVFVIELLQVDAPS
 DYQRETWNLSNHEKMKAVPVLHGEGNRLFKLGRYEEASSKYQEAIICLRNLQTKEKPW
 EVQWLKLEKMINTLILNYCQCLLKKEEYYEVLEHTSDILRHHPGIVKAYYVRARAHAE
 VWNEAEAKADLQKVLELEPSMQKAVRRELRLLENRMAEKQEEERLXCRNMLSQGATQP
 PAEPPTEPPAQSSTEPPAEPPTAPSAELSAGPPAEPATEPPPSPGHSLQH
 - (2) INFORMATION FOR SEQ ID NO:73:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Chimpansee Aipl1
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEOUENCE DESCRIPTION: SEQ ID NO:73:
 - MDAALLLNVEGVKKTILHGGTGELPNFITGSRVIFHFRTMKCDEERTVIDDSRQVGQPMHIIIGN
 MFKLEVWEILLTSMRVHEVAEFWCDTIHTGVYPILSRSLRQMAQGKDPTEWHVHTCGLANMFAYH
 TLGYEDLDELQKEPQPLVFVIELLQVDAPSDYQRETWNLSNHEKMKAVPVLHGEGNRLFKLGRYE
 EASSKYQEAIICLRNLQTKEKPWEVQWLKLEKMINTLILNYCQCLLKKEEYYEVLEHTSDILRHH
 PGIVKAYYVRARAHAEVWNEAEAKADLRKVLELEPSMQKAVRRELRLLENRMAEKQEEERLRCRN
 MLSQGATQPPAEPPTEPPAQSSTEPPAEPPPAPSAELSAGPPAETATEPPPSPGHSLQH
 - (2) INFORMATION FOR SEQ ID NO:74:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids
 - (B) TYPE: amino acid

- (ix) FEATURE:
 - (A) NAME/KEY: Baboon Aipl1
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

MDAALLLNVEGVKKTILHGGTGELPNFITGSRVIFHFRTMKCDEERTVIDDSRQVDQPMHIIIGN MFKLEVWEILLTSMRVHEVAEFWCDTIHTGVYPILSRSLRQMAQGKDPTEWHVHTCGLANMFAYH TLGYEDLDELOKEPOPLIFVIELLQVDAPSDYQRETWNLSNHEKMKVVPVLHGEGNRLFKLGRYE EASSKYQEAIICLRNLQTKEKPWEVQWLKLEKMINTLTLNYCQCLLKKEEYYEVLEHTSDILRHH PGIVKAYYVRARAHAEVWNEAEAKADLQKVLELEPSMQKAVRRELRLLENRMAEKQEEERLRCRN MLSQGATQPPTEPPAEPHTAPPAELSTGPPAEPPAELPLSPGHSLQH

- (2) INFORMATION FOR SEQ ID NO:75:
 - (i) SEOUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Cow Aipl1
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

MDATLLLNVEGIKKTILHGGTGDLPNFITGARVTFHFRTMKCDEERTVIDDSKQVGHPMHIIIGN MFKLEVWEILLTSMRVSEVAEFWCDTIHTGVYPILSRSLRQMAEGKDPTEWHVHTCGLANMFAYH TLGYEDLDELQKEPQPLIFIIELLQVEAPSQYQRETWNLNNQEKMQAVPILHGEGNRLFKLGRYE EASNKYQEAIVCLRNLQTKEKPWEVQWLKLEKMINTLILNYCQCLLKKEEYYEVLEHTSDILRHH PGIVKAYYVRARAHAEVWNEAEAKADLEKVLELEPSMRKAVQRELRLLENRLEEKREEERLRCRN MLG

- (2) INFORMATION FOR SEQ ID NO:76:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids

Page 119

25

30

5

10

- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:

10

25

30

- (A) NAME/KEY: Mouse Aipl1
- (B) LOCATION:
- (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

MDVSLLLNVEGVKKTILHGGTGELPNFITGSRVTFHFRTMKCDEERTVIDDSKQVGQPMSIIIGN
MFKLEVWETLLTSMRLGEVAEFWCDTIHTGVYPMLSRSLRQVAEGKDPTSWHVHTCGLANMFAYH
TLGYEDLDELQKEPQPLVFLYELLQVEAPNEYQRETWNLNNEERMQAVPLLHGEGNRLYKLGRYD
QAATKYQEAIVCLRNLQTKEKPWEVEWLKLEKMINTLILNYCQCLLKKEEYYEVLEHTSDILRHH
PGIVKAYYMRARAHAEVWNAEEAKADLEKVLELEPSMRKAVLRELRLLESRLADKQEEERQRCRS
MLG

- (2) INFORMATION FOR SEQ ID NO:77:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (ix) FEATURE:
 - (A) NAME/KEY: Rhesus Monkey Aipl1
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

MDAALLLNVEGVKKTILHGGTGELPNFITGSRVIFHFRTMKCDEERTVIDDSRQVDQPMHIIIGN
MFKLEVWEILLTSMRVHEVAEFWCDTIHTGVYPILSRSLRQMAQGKDPTEWHVHTCGLANMFAYH
TLGYEDLDELQKEPQPLIFVIELLQVDAPSDYQRETWNLSNHEKMKVVPVLHGEGNRLFKLGRYE
EASSKYQEAIICLRNLQTKEKPWEVQWLKLEKMINTLTLNYCQCLLKKEEYYEVLEHTSDILRHH
PGIVKAYYVRARAHAEVWNEAEAKADLQKVLELEPSMQKAVRRELRLLENRMAEKQEEERLRCRN
MLSQGATQPPAEPPAQPPTAPPAELSTGPPADPPAEPPTAPPAELSTGPPAEPPAELPLSPGHSLQH

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 444 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (ix) FEATURE:
 - (A) NAME/KEY: Squirrel Monkey Aipl1
 - (B) LOCATION:
 - (D) OTHER INFORMATION:
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

MDAALLLNVEGVKKTILHGGTGELPNFITGSRVIFHFRTMKCDEERTVIDDSREVGQPMHIIIGN MFKLEVWEILLTSMRVREVAEFWCDTIHTGVYPILSRSLRQMAQGKDPTEWHVHTCGLANMFAYH TLGYEDLDELQKEPQPLIFVIELLQVDAPSDYQRETWNLSNHEKMKVVPVLHGEGNRLFKLGRYE EASSKYQEAIICLRNLQTKEKPWEVQWLKLEKMINTLILNYCQCLLKKEEYYEVLEHTSDILRHH PGIVKAYYVRARAHAEVWNEAEAKADLQKVLELEPSMQKAVRRELRLLENRMAEKQEEERLRCRN MLSQGATWSPAEPPAEPPAEPPAEPPAEPPAEPPAELTLTPGHPLQH